	gca Ala				-				_	_		_				528
-	gta Val	_			_		_				_			_	aat Asn	576
	ccg Pro			_	_				_			_	_		_	624
_	ctt Leu 210		_	_		_	_				_			_		672
	gcg Ala		_	_						_	_					720
_	gaa Glu	_	_					_				_				768
	ttc Phe	_	_	_		_					_			_	cac His	816
	act Thr			_		_				_	_					864
_	atc Ile 290												_			912
	gcc Ala	_		_	_											960
	gga Gly			_			_			_	_		_	_		1008
	gtc Val	_								-				-	tca Ser	1056
_	gaa Glu				_		-	-			-			_		1104
	tat Tyr 370	-	_		-	_	_					_		_		1152
	tat Tyr															1200
gta	ggc	cag	cat	caa	atg	tgg	tca	gcg	caa	ttt	tat	ccg	ttc	caa	aaa	1248

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Val Gly	/ Gln	His	Gln 405	Met	Trp	Ser	Ala	Gln 410	Phe	Tyr	Pro	Phe	Gln 415	Lys	
gca gat Ala Asp			_	-						-	_				1296
ctt ccc Leu Pro		Ala			_	-	_	_	-		-	_		_	1344
gtc gcg Val Ala 450	a Val	_		_		_									1392
gat gtt Asp Val 465		_	_				_	-	_	-					1440
aac gct Asn Ala	_			_	_	_	_		-	_				_	1488
gaa cgt Glu Arg			-				_		-		_		_		1536
ttg tco Leu Sei	_	Āla							_				_		1584
gaa gca Glu Ala 530	a Lys	_	_	-	-		_				_			_	1632
gtc att Val Ile 545	-				_	_	_			_		_	_		1680
gct ccq Ala Pro				-		-							tga		1725
<210> 32 <211> 574 <212> PRT <213> Bacillus subtilis															
<400> 3 Met Gly		Asn	Val 5	Gln	Val	Asp	Ser	Ala 10	Ser	Ala	Glu	Cys	Thr 15	Gln	
ml - M	0 -	<b>0</b> 3 -	70.7	т	7. f l	<b>-</b>	тз.	0.7	<u> </u>	7	Τ	т	$\sim$ 7	т	

Thr Met Ser Gly Ala Leu Met Leu Ile Glu Ser Leu Lys Lys Glu Lys 20 25 30

Val Glu Met Ile Phe Gly Tyr Pro Gly Gly Ala Val Leu Pro Ile Tyr 35 40 45

Asp Lys Leu Tyr Asn Ser Gly Leu Val His Ile Leu Pro Arg His Glu 50 60

Gln Gly Ala Ile His Ala Ala Glu Gly Tyr Ala Arg Val Ser Gly Lys
65 70 75 80

Pro Gly Val Val Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val 85 90 95

Thr Gly Leu Ala Asp Ala Met Ile Asp Ser Leu Pro Leu Val Val Phe 100 105 110

Thr Gly Gln Val Ala Thr Ser Val Ile Gly Ser Asp Ala Phe Gln Glu 115 120 125

Ala Asp Ile Leu Gly Ile Thr Met Pro Val Thr Lys His Ser Tyr Gln 130 135 140

Val Arg Gln Pro Glu Asp Leu Pro Arg Ile Ile Lys Glu Ala Phe His 145 150 155 160

Ile Ala Thr Thr Gly Arg Pro Gly Pro Val Leu Ile Asp Ile Pro Lys 165 170 175

Asp Val Ala Thr Ile Glu Gly Glu Phe Ser Tyr Asp His Glu Met Asn 180 185 190

Leu Pro Gly Tyr Gln Pro Thr Thr Glu Pro Asn Tyr Leu Gln Ile Arg
200 205

Lys Leu Val Glu Ala Val Ser Ser Ala Lys Lys Pro Val Ile Leu Ala 210 215 220

Gly Ala Gly Val Leu His Gly Lys Ala Ser Glu Glu Leu Lys Asn Tyr 225 230 235 240

Ala Glu Gln Gln Ile Pro Val Ala His Thr Leu Leu Gly Leu Gly 255

Gly Phe Pro Ala Asp His Pro Leu Phe Leu Gly Met Ala Gly Met His 260 265 270

Gly Thr Tyr Thr Ala Asn Met Ala Leu His Glu Cys Asp Leu Leu Ile 275 280 285

Ser Ile Gly Ala Arg Phe Asp Asp Arg Val Thr Gly Asn Leu Lys His 290 295 300

Phe Ala Arg Asn Ala Lys Ile Ala His Ile Asp Ile Asp Pro Ala Glu 305 310 315 320

Ile Gly Lys Ile Met Lys Thr Gln Ile Pro Val Val Gly Asp Ser Lys 325 330 335

Ile Val Leu Gln Glu Leu Ile Lys Gln Asp Gly Lys Gln Ser Asp Ser 340 345 350

Ser Glu Trp Lys Lys Gln Leu Ala Glu Trp Lys Glu Glu Tyr Pro Leu 355 360 365

Trp Tyr Val Asp Asn Glu Glu Glu Gly Phe Lys Pro Gln Lys Leu Ile 370 375 380